

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/525,726  
Source: PG1/10  
Date Processed by STIC: 3/8/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/525,726

DATE: 03/08/2005

TIME: 08:05:11

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03082005\J525726.raw

and

3 <110> APPLICANT: Von Der Kammer, Heinz  
 4 Pohlner, Johannes  
 6 <120> TITLE OF INVENTION: Diagnostic and Therapeutic Use of FOAP-13 Polynucleotides  
 7 Polypeptides for Neurodegenerative Diseases  
 9 <130> FILE REFERENCE: 2335.0060001  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/525,726  
 C--> 12 <141> CURRENT FILING DATE: 2005-02-28  
 14 <150> PRIOR APPLICATION NUMBER: 02019281.1  
 15 <151> PRIOR FILING DATE: 2002-08-28  
 17 <150> PRIOR APPLICATION NUMBER: 60/406,303  
 18 <151> PRIOR FILING DATE: 2002-08-28  
 20 <160> NUMBER OF SEQ ID NOS: 18  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 390  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA fragment  
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 33 <400> SEQUENCE: 1  
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 35 aagaggagca gacagggttc cctgggcccc gtctcagccc agccactgat gctggatgac 120  
 36 cttggcctga ccctgggtctg gtctcagaat cacttttccc atctgtaaaa ttgagatgaa 180  
 37 ttttggtggt gaaagttctt cctggagcag atgtcctaga aggttttagg aatagtgaca 240  
 38 gagtcaggcc accccaaggg ccatgggagc cagctgacct gcttgaccga aggatttctg 300  
 39 acagactatc tttggggatg ttttcaagaa gggatataag ttatttactt tgggcattta 360  
 40 aaagaaaatt tctctcgga ataattttat 390  
 43 <210> SEQ ID NO: 2  
 44 <211> LENGTH: 491  
 45 <212> TYPE: PRT  
 46 <213> ORGANISM: Homo sapiens  
 48 <400> SEQUENCE: 2  
 49 Met Ala Gly Gln Gly Leu Pro Leu His Val Ala Thr Leu Leu Thr Gly  
 50 1 5 10 15  
 52 Leu Leu Glu Cys Leu Gly Phe Ala Gly Val Leu Phe Gly Trp Pro Ser  
 53 20 25 30  
 55 Leu Val Phe Val Phe Lys Asn Glu Asp Tyr Phe Lys Asp Leu Cys Gly  
 56 35 40 45  
 58 Pro Asp Ala Gly Pro Ile Gly Asn Ala Thr Gly Gln Ala Asp Cys Lys  
 59 50 55 60  
 61 Ala Gln Asp Glu Arg Phe Ser Leu Ile Phe Thr Leu Gly Ser Phe Met  
 62 65 70 75 80

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64 Asn Asn Phe Met Thr Phe Pro Thr Gly Tyr Ile Phe Asp Arg Phe Lys
65      85      90      95
67 Thr Thr Val Ala Arg Leu Ile Ala Ile Phe Phe Tyr Thr Thr Ala Thr
68      100      105      110
70 Leu Ile Ile Ala Phe Thr Ser Ala Gly Ser Ala Val Leu Leu Phe Leu
71      115      120      125
73 Ala Met Pro Met Leu Thr Ile Gly Gly Ile Leu Phe Leu Ile Thr Asn
74      130      135      140
76 Leu Gln Ile Gly Asn Leu Phe Gly Gln His Arg Ser Thr Ile Ile Thr
77 145      150      155      160
79 Leu Tyr Asn Gly Ala Phe Asp Ser Ser Ser Ala Val Phe Leu Ile Ile
80      165      170      175
82 Lys Leu Leu Tyr Glu Lys Gly Ile Ser Leu Arg Ala Ser Phe Ile Phe
83      180      185      190
85 Ile Ser Val Cys Ser Thr Trp His Val Ala Arg Thr Phe Leu Leu Met
86      195      200      205
88 Pro Arg Gly His Ile Pro Tyr Pro Leu Pro Pro Asn Tyr Ser Tyr Gly
89      210      215      220
91 Leu Cys Pro Gly Asn Gly Thr Thr Lys Glu Glu Lys Glu Thr Ala Glu
92 225      230      235      240
94 His Glu Asn Arg Glu Leu Gln Ser Lys Glu Phe Leu Ser Ala Lys Glu
95      245      250      255
97 Glu Thr Pro Gly Ala Gly Gln Lys Gln Glu Leu Arg Ser Phe Trp Ser
98      260      265      270
100 Tyr Ala Phe Ser Arg Arg Phe Ala Trp His Leu Val Trp Leu Ser Val
101      275      280      285
103 Ile Gln Leu Trp His Tyr Leu Phe Ile Gly Thr Leu Asn Ser Leu Leu
104      290      295      300
106 Thr Asn Met Ala Gly Gly Asp Met Ala Arg Val Ser Thr Tyr Thr Asn
107 305      310      315      320
109 Ala Phe Ala Phe Thr Gln Phe Gly Val Leu Cys Ala Pro Trp Asn Gly
110      325      330      335
112 Leu Leu Met Asp Arg Leu Lys Gln Lys Tyr Gln Lys Glu Ala Arg Lys
113      340      345      350
115 Thr Gly Ser Ser Thr Leu Ala Val Ala Leu Cys Ser Thr Val Pro Ser
116      355      360      365
118 Leu Ala Leu Thr Ser Leu Leu Cys Leu Gly Phe Ala Leu Cys Ala Ser
119      370      375      380
121 Val Pro Ile Leu Pro Leu Gln Tyr Leu Thr Phe Ile Leu Gln Val Ile
122 385      390      395      400
124 Ser Arg Ser Phe Leu Tyr Gly Ser Asn Ala Ala Phe Leu Thr Leu Ala
125      405      410      415
127 Phe Pro Ser Glu His Phe Gly Lys Leu Phe Gly Leu Val Met Ala Leu
128      420      425      430
130 Ser Ala Val Val Ser Leu Leu Gln Phe Pro Ile Phe Thr Leu Ile Lys
131      435      440      445
133 Gly Ser Leu Gln Asn Asp Pro Phe Tyr Val Asn Val Met Phe Met Leu
134      450      455      460
136 Ala Ile Leu Leu Thr Phe Phe His Pro Phe Leu Val Tyr Arg Glu Cys

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137 465                               470                               475                               480
139 Arg Thr Trp Lys Glu Ser Pro Ser Ala Ile Ala
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145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA of the
150     human foap-13 gene
152 <400> SEQUENCE: 3
153 cggacgcgtg ggcggacgcg tggcggaagc cgtgggctct gggagtgtga aactgggaga 60
154 gacgggttaag ctggggacgg tattcagaat tcgagcgcag gagctccgct tctccacctg 120
155 ctcccgggga gctattggga tccagagaat caccgcgtga tggtttttcc ccaggcctga 180
156 aacaaccaga gagctacggg aaaggaaggg cttggccttg cagaggaatt ttccaagtgc 240
157 tcaaacgcca ggcttacggc gcctgtgatc cgtccaggag gacaaagtgg gatttgaaga 300
158 tccactccac ttctgtcat ggcgggccag ggcctgcccc tgcacgtggc cacactgctg 360
159 actgggctgc tggaaatgcct gggcttttgc ggcgtcctct ttggctggcc ttcactagt 420
160 tttgtcttca agaatagaaga ttactttaag gatctgtgtg gaccagatgc tgggcccatt 480
161 ggcaatgcca cagggcaggc tgactgcaaa gcccaggatg agaggttctc actcatcttc 540
162 accctggggc ctttcatgaa caacttcatg acattcccca ctggctacat ctttgaccgg 600
163 ttcaagacca ccgtggcacg cctcatagcc atatttttct acaccaccgc cacactcatc 660
164 atagccttca cctctgcagg ctccagccgt ctgctcttcc tggccatgcc aatgctcacc 720
165 attgggggaa tcctgtttct catcaccaac ctgcagattg ggaacctatt tggccaacac 780
166 cgttcgacca tcatcactct gtacaatgga gcatttgact ctctctcggc agtcttcctt 840
167 attattaagc ttctttatga aaaaggcatc agcctcaggg cctccttcat ctctcatctc 900
168 gtctgcagta cctggcatgt agcacgcaat ttctctctga tgccccgggg gcacatccca 960
169 taccactgca cccccaaacta cagctatggc ctgtgccctg ggaatggcac cacaaggaa 1020
170 gagaaggaaa cagctgagca tgaaaacagg gagctacagt caaaggagtt cttttcagcg 1080
171 aaggaagaga ccccgagggc agggcagaag caggaaactc gctccttctg gagctacgct 1140
172 ttctctcggc gctttgcctg gcacctggtg tggctgtctg tgatacagtt gtggcactac 1200
173 ctcttcattg gcaactctca ctcttgcctg accaaccatg ccggtgggga catggcacga 1260
174 gtacagcact acacaaatgc ctttgccttc actcagttcg gagtgctgtg tgccccctgg 1320
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176 tcctccactt tggcggtggc cctctgctcg acggtgcctt cgctggccct gacatccctg 1440
177 ctgtgcctgg gcttgcctct ctgtgcctca gtcccatcc tccctctcca gtacctcacc 1500
178 ttcatcctgc aagtgatcag ccgctccttc ctctatggga gcaacgcggc ctctctcacc 1560
179 cttgctttcc cttcagagca ctttggcaag ctctttgggc tggatgatgg cttgtcggct 1620
180 gtggtgtctc tgctccagtt ccccatcttc accctcatca aaggctccct tcagaatgac 1680
181 ccattttacg tgaatgtgat gttcatgctt gccattcttc tgacattctt ccacctctt 1740
182 ctggtatata gggaaatgcc tacttggaaa gaaagtcct ctgcaattgc atagttcaga 1800
183 agcctcact tttcagcccc gaggatggtt ttgttcatct tccaccacct ttgaggacct 1860
184 cgtgtcccaa aagactttgc ctatcccagc aaaacacaca cacacacaca cacacacaca 1920
185 aaataaagac acacaaggac gtctgcgcag caagaaaaga atctcagttg ccaagcagat 1980
186 tgatatcaca cagactcaaa gcaaaggcat gtggaacttc tttatttcaa aacagaagt 2040
187 tctccttgca cttagccttg gcagaccctt gactccaggg gagatgacct gggggaggaa 2100
188 gtgtgtcaac tatttcttta ggcctgtttg gctccgaagc ctatatgtgc ctggatcctc 2160
189 tgccacgggt taaattttca ggtgaagagt gaggttgtca tggcctcagc tatgcttctc 2220
190 ggctctccct caagagtgca gccttggcta gagaactcac agctctggga aaaagaggag 2280

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191 cagacagggt tccctgggcc cagtctcagc ccagccactg atgctggatg accttggcct 2340
192 gaccctggtc tggctcaga atcacttttc ccatctgtaa aattgagatg aattttggtg 2400
193 ttgaaagtgc ttcctggagc agatgtccta gaaggtttta ggaatagtga cagagtcagg 2460
194 ccacccaag ggccatggga gccagctgac ctgcttgacc gaaggatttc tgacagacta 2520
195 tctttgggga tgttttcaag aagggatata agttatttac tttgggcatt taaaagaaaa 2580
196 tttctctcgg gaataatttt atagaaaaat aaagcttctg tgtctaaggc 2630
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200 <211> LENGTH: 13
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Description of Artificial Sequence: one-base
206     anchor oligonucleotide
208 <400> SEQUENCE: 4
209 httttttttt tta 13
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 13
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: One-base
219     anchor oligonucleotide
221 <400> SEQUENCE: 5
222 httttttttt ttg 13
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 13
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence: One-base
232     anchor oligonucleotide
234 <400> SEQUENCE: 6
235 httttttttt ttc 13
238 <210> SEQ ID NO: 7
239 <211> LENGTH: 23
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
245     foap-13 gene
247 <400> SEQUENCE: 7
248 tcaggtgaag agtgaggttg tca 23
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
258     foap-13 gene

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Input Set : A:\PTO.SR.txt

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265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
271     cyclophilin B gene
273 <400> SEQUENCE: 9
274 actgaagcac tacgggcctg                                20
277 <210> SEQ ID NO: 10
278 <211> LENGTH: 19
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
284     cyclophilin B gene
286 <400> SEQUENCE: 10
287 agccggttggt gtctttgcc                                19
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291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
297     ribosomal protein S9
299 <400> SEQUENCE: 11
300 ggtcaaattt accctggcca                                20
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304 <211> LENGTH: 22
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
310     ribosomal protein S9
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313 tctcatcaag cgtcagcagt tc                                22
316 <210> SEQ ID NO: 13
317 <211> LENGTH: 19
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence: primer for the
323     beta-actin gene
325 <400> SEQUENCE: 13
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329 <210> SEQ ID NO: 14
330 <211> LENGTH: 19

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## VERIFICATION SUMMARY

DATE: 03/08/2005

PATENT APPLICATION: US/10/525,726

TIME: 08:05:12

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Output Set: N:\CRF4\03082005\J525726.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date